

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2002, 06:41:09 ; Search time 1759.97 Seconds
(without alignments)
187.471 Million cell updates/sec

Title: US-08-887-505-117

Perfect score: 20
Sequence: 1 TTNGCGACCCCACTACTC 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_om:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pl:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_sy:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htgo_hum:*
- 31: em_htgo_inv:*
- 32: em_htgo_rod:*
- 33: em_htgo_hum:*
- 34: em_htg_inv:*
- 35: em_htg_rod:*
- 36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	95.0	27	6	AR106359 Sequence
C 2	19	95.0	33	6	AR004396 Sequence
C 3	19	95.0	33	6	AR064935 Sequence
C 4	19	95.0	33	6	AR097188 Sequence
C 5	19	95.0	33	6	AR130686 Sequence
C 6	19	95.0	33	6	AR128711 Sequence 50
C 7	19	95.0	33	6	AR153179 Sequence
C 8	19	95.0	40	6	AR153179 Sequence
C 9	19	95.0	46	6	I44581 Sequence 10
C 10	19	95.0	46	6	I70986 Sequence 10
C 11	19	95.0	139	14	AF282631 Hepatitis
C 12	19	95.0	139	14	AF282632 Hepatitis
C 13	19	95.0	139	14	AF282633 Hepatitis
C 14	19	95.0	139	14	AF282634 Hepatitis
C 15	19	95.0	139	14	AF282635 Hepatitis
C 16	19	95.0	139	14	AF282637 Hepatitis
C 17	19	95.0	139	14	AF282638 Hepatitis
C 18	19	95.0	139	14	AF282639 Hepatitis
C 19	19	95.0	139	14	AF282640 Hepatitis
C 20	19	95.0	139	14	AF282641 Hepatitis
C 21	19	95.0	139	14	AF282642 Hepatitis
C 22	19	95.0	139	14	AF282643 Hepatitis
C 23	19	95.0	139	14	AF282644 Hepatitis
C 24	19	95.0	139	14	AF282645 Hepatitis
C 25	19	95.0	139	14	AF282646 Hepatitis
C 26	19	95.0	139	14	AY003921 Hepatitis
C 27	19	95.0	139	14	AY003922 Hepatitis
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C 29	19	95.0	139	14	AY003924 Hepatitis
C 30	19	95.0	139	14	AY003925 Hepatitis
C 31	19	95.0	139	14	AY003928 Hepatitis
C 32	19	95.0	139	14	AY003929 Hepatitis
C 33	19	95.0	139	14	AY003930 Hepatitis
C 34	19	95.0	139	14	AY003932 Hepatitis
C 35	19	95.0	139	14	AY003933 Hepatitis
C 36	19	95.0	139	14	AY003934 Hepatitis
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C 38	19	95.0	139	14	AY003936 Hepatitis
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C 41	19	95.0	139	14	AY003939 Hepatitis
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ALIGNMENTS

RESULT 1
LOCUS AR106359/c 27 bp DNA
DEFINITION Sequence 21 from patent US 6107028.
ACCESSION AR106359
VERSION AR106359.1 GI:12820889
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kay, M.A. and Lieber, A.
TITLE Ribozymes for treating hepatitis C
JOURNAL Patent: US 6107028-A 21 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..27
BASE COUNT 6 a 4 c 12 g 5 t
ORIGIN

14-FEB-2001

PAT

Fri Jan 11 09:31:11 2002

us-08-887-505-117.rge

Page 2

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Best Local Similarity 95.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 24 TTTCGCGACCCCAACTACTC 5

RESULT 2
LOCUS AR004396
DEFINITION Sequence 33 bp DNA
ACCESSION AR004396
VERSION AR004396
KEYWORDS 04-DEC-1998
SOURCE PAT
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan, P., Chang, C., Running, J. and Urdea, M.S.
TITLE Nucleic acid probes immobilized on polystyrene surfaces
JOURNAL Patent: US 5747244-A 50 05-MAY-1998;
FEATURES Location/Qualifiers
source 1..33
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN /organism="unknown"

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Best Local Similarity 95.0%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCGCGACCCCAACTACTC 20
DB 10 TTTCGCGACCCCAACTACTC 29

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LOCUS AR064935
DEFINITION Sequence 33 bp DNA
ACCESSION AR064935
VERSION AR064935
KEYWORDS 29-SEP-1998
SOURCE PAT
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Urdea, M.S., Horn, T., Chang, C., Warner, B. and Fu
TITLE Nucleic acid hybridization assays employing lar
JOURNAL branched polynucleotides
FEATURES Patent: US 5849481-A 60 15-DEC-1998;
source Location/Qualifiers
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BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN /organism="unknown"

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RESULT 4
LOCUS AR097188

LOCUS AR097188
DEFINITION Sequence 33 bp DNA
ACCESSION AR097188
VERSION AR097188
KEYWORDS 14-FEB-2001
SOURCE PAT
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6071693-A 126 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..33
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN /organism="unknown"

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Best Local Similarity 95.0%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 10 TTTCGCGACCCCAACTACTC 29

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DEFINITION Sequence 33 bp DNA
ACCESSION AR130686
VERSION AR130686
KEYWORDS 16-MAY-2001
SOURCE PAT
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6190864-A 126 20-FEB-2001;
FEATURES Location/Qualifiers
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BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN /organism="unknown"

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DB 10 TTTCGCGACCCCAACTACTC 29

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LOCUS R82871
DEFINITION Sequence 50 from patent US 5712383.
ACCESSION R82871
VERSION R82871
KEYWORDS 10-JUN-1998
SOURCE PAT
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan, P., Chang, C., Running, J. and Urdea, M.S.
TITLE process for immobilizing nucleic acid probes on surfaces


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AUTHORS      Harris,K.A. and Teo,C.G.
TITLE        Direct Submission
JOURNAL       Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
              Central Public Health Laboratory, 61 Colindale Avenue, London NW9
              5HT, UK

FEATURES
  source      Location/Qualifiers
              1. .139
                /organism="Hepatitis C virus"
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 116 TTGCGACCCCAACTACTC 97

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LOCUS       AF282634            139 bp    RNA                VRL             01-MAR-2001
DEFINITION  Hepatitis C virus isolate H071 clone II 5' non-coding region
ACCESSION   AF282634
VERSION     AF282634.1   GI:10764497
KEYWORDS    .
SOURCE      Hepatitis C virus.
ORGANISM    Hepatitis C virus.
REFERENCE   1 (bases 1 to 139)
            Harris,K.A. and Teo,C.G.
            Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
            Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
            11139197
REFERENCE   2 (bases 1 to 139)
            Harris,K.A. and Teo,C.G.
            Direct Submission
            Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK

FEATURES
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              1. .139
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  misc_feature 1. .139
                /note="5' non-coding region"
BASE COUNT    27 a 38 c 43 g 31 t
ORIGIN
Query Match   95.0%; Score 19; DB 14; Length 139;
Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
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Db 116 TTGCGACCCCAACTACTC 97

RESULT 14
AF282635/c

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LOCUS AF282635 139 bp RNA VRL 01-MAR-2001
DEFINITION Hepatitis C virus isolate H075 clone I 5' non-coding region
sequence.
ACCESSION AF282635
VERSION AF282635.1 GI:10764498
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES
source Location/Qualifiers
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/organism="Hepatitis C virus"
/isolate="H075"
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Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTNGCGACCCCAACTACTC 20
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Db 116 TTGCGACCCCAACTACTC 97

RESULT 15
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LOCUS AF282637 139 bp RNA VRL 01-MAR-2001
DEFINITION Hepatitis C virus isolate H075 clone III 5' non-coding region
sequence.
ACCESSION AF282637
VERSION AF282637.1 GI:10764500
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES
source Location/Qualifiers
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BASE COUNT 26 a 36 c 44 g 33 t
ORIGIN

Query Match 95.0%; Score 19; DB 14; Length 139;
Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTNGCGACCCCAACTACTC 20
|||
Db 116 TTGCGACCCCAACTACTC 97

Search completed: January 11, 2002, 06:41:09
Job time: 9725 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2002, 06:41:09 ; Search time 1759.97 Seconds
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Title: US-08-887-505-118
Perfect score: 20
Sequence: 1 TTGCGNACCAACNCTACTC 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.hig.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vl.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.om.*
- 20: em.or.*
- 21: em.ov.*
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- 25: em.ro.*
- 26: em.sts.*
- 27: em.sy.*
- 28: em.un.*
- 29: em.vl.*
- 30: em.htgo_hum.*
- 31: em.htgo_inv.*
- 32: em.htgo_rod.*
- 33: em.htg_hum.*
- 34: em.htg_inv.*
- 35: em.htg_rod.*
- 36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
1	18	90.0	23	6	I73297	I73297 Sequence 28
c 2	18	90.0	27	6	ARI06359	ARI06359 Sequence
3	18	90.0	33	6	AR004396	AR004396 Sequence
4	18	90.0	33	6	AR064935	AR064935 Sequence
5	18	90.0	33	6	AR097188	AR097188 Sequence
6	18	90.0	33	6	AR130686	AR130686 Sequence
c 7	18	90.0	33	6	I73295	I73295 Sequence 26
8	18	90.0	33	6	I82871	I82871 Sequence 50
c 9	18	90.0	40	6	ARI53179	ARI53179 Sequence
10	18	90.0	46	6	I44581	I44581 Sequence 10
11	18	90.0	46	6	I70986	I70986 Sequence 10
12	18	90.0	53	6	I44619	I44619 Sequence 48
13	18	90.0	53	6	I71024	I71024 Sequence 48
c 14	18	90.0	57	6	I73305	I73305 Sequence 36
15	18	90.0	64	6	I44601	I44601 Sequence 30
16	18	90.0	64	6	I71006	I71006 Sequence 30
c 17	18	90.0	138	14	HC081281	HC081281 Hepatitis C
c 18	18	90.0	139	14	AF282631	AF282631 Hepatitis
c 19	18	90.0	139	14	AF282632	AF282632 Hepatitis
c 20	18	90.0	139	14	AF282633	AF282633 Hepatitis
c 21	18	90.0	139	14	AF282634	AF282634 Hepatitis
c 22	18	90.0	139	14	AF282635	AF282635 Hepatitis
c 23	18	90.0	139	14	AF282636	AF282636 Hepatitis
c 24	18	90.0	139	14	AF282637	AF282637 Hepatitis
c 25	18	90.0	139	14	AF282638	AF282638 Hepatitis
c 26	18	90.0	139	14	AF282639	AF282639 Hepatitis
c 27	18	90.0	139	14	AF282640	AF282640 Hepatitis
c 28	18	90.0	139	14	AF282641	AF282641 Hepatitis
c 29	18	90.0	139	14	AF282642	AF282642 Hepatitis
c 30	18	90.0	139	14	AF282643	AF282643 Hepatitis
c 31	18	90.0	139	14	AF282644	AF282644 Hepatitis
c 32	18	90.0	139	14	AF282645	AF282645 Hepatitis
c 33	18	90.0	139	14	AF282646	AF282646 Hepatitis
c 34	18	90.0	139	14	AY003921	AY003921 Hepatitis
c 35	18	90.0	139	14	AY003922	AY003922 Hepatitis
c 36	18	90.0	139	14	AY003923	AY003923 Hepatitis
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c 43	18	90.0	139	14	AY003932	AY003932 Hepatitis
c 44	18	90.0	139	14	AY003933	AY003933 Hepatitis
c 45	18	90.0	139	14	AY003934	AY003934 Hepatitis

ALIGNMENTS

RESULT 1

I73297

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

I73297 Sequence 28 from patent US 5686272.

I73297

I73297.1 GI:3009436

Unknown.

Unclassified.

1 (bases 1 to 23)

Marshall, R.L., Carrino, J.J. and Sustachek, J.C.

Amplification of RNA sequences using the ligase chain reaction

Patent: US 5686272-A 28 11-NOV-1997;

Location/Qualifiers

1..23

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PAT 03-APR-1998

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Db 2 TTTCGCAACCCACACTACTC 21

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AR106359/c AR106359 27 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 21 from patent US 6107028.
ACCESSION AR106359
VERSION AR106359.1 GI:12820889
KEYWORDS
SOURCE Unknown.

REFERENCE Unclassified.
1 (bases 1 to 27)
AUTHORS Kay, M.A. and Lieber, A.
TITLE Ribozymes for treating hepatitis C
JOURNAL Patent: US 6107028-A 21 22-AUG-2000;
FEATURES Location/Qualifiers
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ORIGIN

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AR004396 AR004396 33 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 50 from patent US 5747244.
ACCESSION AR004396
VERSION AR004396.1 GI:3965275
KEYWORDS
SOURCE Unknown.

REFERENCE Unclassified.
1 (bases 1 to 33)
AUTHORS Sheridan, P., Chang, C., Running, J. and Urdea, M.S.
TITLE Nucleic acid probes immobilized on polystyrene surfaces
JOURNAL Patent: US 5747244-A 50 05-MAY-1998;
FEATURES Location/Qualifiers
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AR064935 AR064935 33 bp DNA PAT 29-SEP-1999
LOCUS

DEFINITION Sequence 60 from patent US 5849481.
ACCESSION AR064935
VERSION AR064935.1 GI:5995151
KEYWORDS
SOURCE Unknown.

REFERENCE Unclassified.
1 (bases 1 to 33)
AUTHORS Urdea, M.S., Horn, T., Chang, C., Warner, B. and Fultz, T.J.
TITLE Nucleic acid hybridization assays employing large comb-type
JOURNAL branched polynucleotides
FEATURES Patent: US 5849481-A 60 15-DEC-1998;
Location/Qualifiers
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BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 33;
Best Local Similarity 90.0%; Pred. No. 9.5;
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QY 1 TTTCGCNACCCACACTACTC 20
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Db 10 TTTCGCGACCCACACTACTC 29

RESULT 5
AR097188 AR097188 33 bp DNA PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 126 from patent US 6071693.
ACCESSION AR097188
VERSION AR097188.1 GI:12805918
KEYWORDS
SOURCE Unknown.

REFERENCE Unclassified.
1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6071693-A 126 06-JUN-2000;
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Db 10 TTTCGCGACCCACACTACTC 29

RESULT 6
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LOCUS
DEFINITION Sequence 126 from patent US 6190864.
ACCESSION AR130686
VERSION AR130686.1 GI:14119011
KEYWORDS
SOURCE Unknown.

REFERENCE Unclassified.
1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6190864-A 126 20-FEB-2001;
FEATURES Location/Qualifiers

source 1..33
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BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 33;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
||||| ||||||| |||||||
Db 10 TTGCGACCCAACTACTC 29

RESULT 7
I73295/c
LOCUS 33 bp DNA PAT 03-APR-1998
DEFINITION Sequence 26 from patent US 5686272.
ACCESSION I73295
VERSION I73295.1 GI:3009434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE Amplification of RNA sequences using the ligase chain reaction
JOURNAL Patent: US 5686272-A 26 11-NOV-1997;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
BASE COUNT. 5 a 4 c 14 g 10 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 33;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
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Db 21 TTGCGACCCAACTACTC 2

RESULT 8
I82871
LOCUS 33 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 50 from patent US 5712383.
ACCESSION I82871
VERSION I82871.1 GI:3211168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
TITLE Process for immobilizing nucleic acid probes on polystyrene surfaces
JOURNAL Patent: US 5712383-A 50 27-JAN-1998;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 33;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
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Db 10 TTGCGACCCAACTACTC 29

RESULT 9
ARI53179/c
LOCUS 40 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 181 from patent US 6235480.
ACCESSION ARI53179
VERSION ARI53179.1 GI:15120711
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Shultz,J.William, Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D., Rhodes,R.Byron, Andrews,C.Ann, Hartnett,J.Robert, Gu,T., Olson,R.J., Wood,K.V. and Welch,R.
TITLE Detection of nucleic acid hybrids
JOURNAL Patent: US 6235480-A 181 22-MAY-2001;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
BASE COUNT 6 a 8 c 16 g 10 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 40;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
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Db 29 TTGCGACCCAACTACTC 10

RESULT 10
I44581
LOCUS 46 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 10 from patent US 5635352.
ACCESSION I44581
VERSION I44581.1 GI:2469294
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 10 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..46
/organism="unknown"
BASE COUNT 9 a 17 c 11 g 9 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 46;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
||||| ||||||| |||||||
Db 10 TTGCGACCCAACTACTC 29

RESULT 11
I70986
LOCUS 46 bp DNA PAT 03-APR-1998
DEFINITION Sequence 10 from patent US 5681697.
ACCESSION I70986
VERSION I70986.1 GI:3007121
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL Patent: US 5681697-A 10 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..46
BASE COUNT 9 a 17 c 11 g 9 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 46;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCGACCCCAACTACTC 20
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Db 10 TTTCGCGACCCCAACTACTC 29

RESULT 12
LOCUS I44619 53 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 48 from patent US 5635352.
ACCESSION I44619
VERSION I44619.1 GI:2469332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 48 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..53
BASE COUNT 13 a 18 c 11 g 11 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 53;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCGACCCCAACTACTC 20
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Db 30 TTTCGCGACCCCAACTACTC 49

RESULT 13
LOCUS I71024 53 bp DNA PAT 03-APR-1998
DEFINITION Sequence 48 from patent US 5681697.
ACCESSION I71024
VERSION I71024.1 GI:3007159
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL Patent: US 5681697-A 48 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..53
BASE COUNT 13 a 18 c 11 g 11 t
ORIGIN

BASE COUNT 13 a 18 c 11 g 11 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 53;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCGACCCCAACTACTC 20
||||| ||||||| |||||||
Db 30 TTTCGCGACCCCAACTACTC 49

RESULT 14
LOCUS I73305/c 57 bp DNA PAT 03-APR-1998
DEFINITION Sequence 36 from patent US 5686272.
ACCESSION I73305
VERSION I73305.1 GI:3009444
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 57)
AUTHORS Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE Amplification of RNA sequences using the ligase chain reaction
JOURNAL Patent: US 5686272-A 36 11-NOV-1997;
FEATURES Location/Qualifiers
source 1..57
BASE COUNT 9 a 9 c 23 g 16 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 57;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCGACCCCAACTACTC 20
||||| ||||||| |||||||
Db 21 TTTCGCGACCCCAACTACTC 2

RESULT 15
LOCUS I44601 64 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 30 from patent US 5635352.
ACCESSION I44601
VERSION I44601.1 GI:2469314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 64)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 30 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..64
BASE COUNT 14 a 25 c 9 g 16 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 64;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCGACCCCAACTACTC 20
||||| ||||||| |||||||
Db 25 TTTCGCGACCCCAACTACTC 44

Search completed: January 11, 2002, 06:41:09
Job time: 9725 sec